Methods: A total of 217 strains of S. pneumoniae obtained from invasive (blood, CSF, pleural fluid) and non-invasive sites (respiratory sites) of both pediatric and adult patients were serotyped by the method of Pai et al (2006). Strains were identified by standard methods and their antibiotic resistance profile determined by agar dilution method (PEN, ERY, CRO, CTX, CXM, CIP, GAT, MOX, LVX) and disk diffusion (PEN, ERY, CRO, CXM, AMC, AMP, VAN, SXT, CL, CN10, DA, OX, CIP). Seven different multiplex PCRs were used to determine the following serotypes/serogroups: 1, 2, 3, 4, 5, 8, 13, 14, 20, 21, 31, 34, 37, 38, 39, 40, 44, 46, 6A, 7A, 7B, 7C, 7F, 9A, 9N, 9L, 9L, 10A, 10F, 11A, 11D, 11F, 12A, 12B, 12F, 15A, 15B, 15C, 15F, 16A, 16F, 17F, 33A,35B, 35F, 35A, 35C, and 47F. The cps operon was used as the internal positive control.

Results: Of the 217 strains, there were 22.6% PRSP, 27.7% PISP and 49.8% PSSP strains based on their susceptibility to penicillin. Serotypes detected were the 19F, 18C, 15B/C, 23F, 6A/B, 10A, 12A/F, 3, 14, 11A/D, 34, 19A, 16F, 35F/47F, and 7F/A. The most predominant serotype was 19F and it was also predominant in isolates obtained from invasive sites. Serotype 19F and 23F were observed to be common among the PRSP strains, with 35/49 strains serotyped as 19F while 13/49 strains were serotyped as 23F. Only one PRSP strain was serotyped as 34. Serotype 19F was also predominant among the PISP strains. Other serotypes detected among the PISP strains were 6A/B, 11A/D, 23F and 14. However, the distribution of these serotypes were rare. The PSSP strains showed to have other serotypes such as 18C, 15B/C, 6A/B, 10A, 19A, 3, 14, 16F, & 7B/C, 7F and 35F/47F. The distribution of serotype 19F and 23F was rare among this group of isolates.

Conclusion: In conclusion, we observe serotype 19F and 23F to be prevalent among the penicillin resistant strains, which has been included in the 7-valent conjugate vaccine. Therefore, the efficacy of this vaccine should be effective in our population. However, it is not possible to predict serotypes that might become predominant in the future.

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44.024

Rapid Consumption of Vancomycin in the Presence of Beta-Lactam Antibiotics Causes Beta-Lactam Antibiotic-Induced Vancomycin-Resistance in Methicillin-resistant Staphylococcus aureus

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Background: One may treat MRSA infections by combination of vancomycin (VCM) with β-lactam antibiotics. Such a combination therapy, however, often causes emergence of VCM-resistant MRSA. The mechanism of this phenomenon, β-lactam antibiotic-induced VCM-resistance (BIVR), is the subject of our investigation to be elucidated. Currently up to 20% of blood isolated MRSA are found to be BIVR strains. Here we report the accelerated consumption of free VCM by the

Methods: A representative BIVR strain, BIVR744 (MIC: VCM 4 mg/L), was selected under various rationale and used throughout the experiments. Free VCM in the medium was quantified by a competitive-ELISA that enabled us to detect the decrease of free VCM at the level of 0.1 μg/mL. Morphological changes of cells grown with VCM and those with VCM+ceftizoxime (CZX) were compared by electron microscopy. Penicillin binding proteins (PBP_S) 2 and 2′ were determined by the fluorescent method.

Results: Growth of BIVR744 in the presence of 4 mg/L VCM took 27 h to reach A578 = 1.0, whereas it was only 8 h under coexistence of 1mg/L CZX. Without CZX, free VCM remained >2.1 mg/L in the first 24 h and the growth was inhibited. On the other hand, in the presence of 1 mg/L CZX, VCM decreased to 0.5 mg/L at 8 h resulting the growth to A578 = 1.44. During inhibited by VCM, thickened cell walls were observed in both cells cultivated with and without CZX, however, the grown cells in the presence of CZX showed normal morphology. CZX showed no effect on the amount of PBP2 and 2′ although BIVR 744 contains large quantities of them.

Conclusion: It was concluded that the BIVR phenomenon is attributable to the accelerated VCM consumption by coexisted β-lactam antibiotics.

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Current Susceptibility Patterns for *Streptococcus pneumoniae* Isolates from Europe and Asia: Findings of the 2007 GLOBAL Surveillance Program

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Background: Resistance (R) to penicillin (PEN), macrolides, and other commonly prescribed agents used to treat community-acquired respiratory tract infections caused by *S. pneumoniae* (SP) has become prevalent. Often, these organisms can be multi-drug resistant (MDR) which is especially problematic for clinicians. Investigation of regional trends in susceptibility (S) patterns and careful consideration of MDR prevalence can provide useful information for empiric treatment. The GLOBAL Surveillance program was designed to monitor the S patterns of SP on a regional level.

Methods: During 2007, 1547 SP were collected from 5 countries in Europe (EU; France [FR], Germany [GE], Italy [IT], Spain [SPN], Belgium [BG], and the United Kingdom [UK] and 554 SP were collected from 4 regions in Asia (AS; Hong Kong [HK], South Korea [SK], China [CH], and Taiwan [TW]). All isolates were centrally tested by broth microdilution (CLSI M7-A7, 2006) against levofloxacin (LFX) and 12 comparator agents. MIC results were interpreted according to CLSI M100-S17, 2007. For SP, MDR was defined as R to ≥2 of the following agents: PEN, cefuroxime (CFX), erythromycin (ERY), tetracycline (TET), and trimethoprim-sulfamethoxazole (SXT).